1: Extremophiles. 1999 Nov;3(4):283-91.

Characterization of an inducible nitrilase from a thermophilic bacillus.

Almatawah QA, Cramp R, Cowan DA.

Department of Biochemistry and Molecular Biology, University College London, UK.

Nitrilase activity was induced in the thermophilic bacterium Bacillus pallidus strain Dac521 by growth on benzonitrile-supplemented minimal medium. The enzyme had a subunit relative molecular mass of 41 kDa but was purified as a complex with a putative GroEL protein (total M(r), 600 kDa). The enzyme catalyzed the hydrolysis of aliphatic, aromatic, and heterocyclic nitriles with widely varying kcat/KM values, primarily the result of differences in substrate affinity. Of the nitriles tested, 4-cyanopyridine was hydrolyzed at the fastest rate. Substitution of benzonitrile at the meta or para position either had no effect on catalytic rate or enhanced kcat, while orthosubstitution was strongly inhibitory, probably because of steric hindrance. The effect of catalytic inhibitors was consistent with the presence of active site thiol residues although activity was little affected by putative thiol reagents such as iodoacetate, iodoacetamide, and N-methylmaleimide. Enzymatic activity was constant between pH 6 and 9 with an optimum at pH 7.6. The optimal temperature for activity was 65 degrees C with rapid activity loss at higher temperatures. The purified nitrilase-GroEL complex had the following half-lives of activity: 8.4 h at 50 degrees C, 2.5 h at 60 degrees C, 13 min at 70 degrees C, and less than 3 min at 80 degrees C.

PMID: 10591020 [PubMed - indexed for MEDLINE]

2: Biochem Biophys Res Commun. 1998 Dec 30;253(3):662-6.

Erratum in:
Biochem Biophys Res Commun 1999 Feb 16;255(2):549.

Nitrilase catalyzes amide hydrolysis as well as nitrile hydrolysis.

Kobayashi M, Goda M, Shimizu S.

Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto
University, Japan.

While amides were reported to be completely inert as substrates for all nitrilases reported to date, the nitrilase from Rhodococcus rhodochrous J1, which catalyzes the hydrolytic cleavage of the C-N triple bond in nitrile to form acid and ammonium, was surprisingly found to catalyze hydrolysis of amide to acid and ammonium stoichiometrically. This nitrilase exhibited a Km of 2.94 mM for benzamide, similar to that for benzonitrile as the original substrate (2.10 mM), but the Vmax for benzamide was six orders of magnitude lower than that for benzonitrile. Benzamide inhibited the nitrilase reaction in a reversible, apparently competitive manner. A mutant nitrilase containing alanine or serine instead of Cys165, which is essential for nitrilase catalytic activity, showed no amidase activity. This observation demonstrated that Cys165

plays a crucial role in the hydrolysis of amides as well as nitriles. Together with some reports that certain nitrilases were previously noted to produce low amounts of amide as a by-product from nitrile, the above unexpected findings suggested the existence of a common tetrahedral intermediate in the nitrilase reaction involving nitrile or amide as a substrate.

PMID: 9918784 [PubMed - indexed for MEDLINE]

3: Protein Sci. 1994 Aug;3(8):1344-6.

A new family of carbon-nitrogen hydrolases.

Bork P, Koonin EV.

European Molecular Biology Laboratory, Heidelberg, Germany.

Using computer methods for database search and multiple alignment, statistically significant sequence similarities were identified between several nitrilases with distinct substrate specificity, cyanide hydratases, aliphatic amidases, beta-alanine synthase, and a few other proteins with unknown molecular function. All these proteins appear to be involved in the reduction of organic nitrogen compounds and ammonia production. Sequence conservation over the entire length, as well as the similarity in the reactions catalyzed by the known enzymes in this family, points to a common catalytic mechanism. The new family of enzymes is characterized by several conserved motifs, one of which contains an invariant cysteine that is part of the catalytic site in nitrilases. Another highly conserved motif includes an invariant glutamic acid that might also be involved in catalysis.

PMID: 7987228 [PubMed - indexed for MEDLINE]

4: Biotechnol Appl Biochem. 1992 Jun;15(3):283-302.

Mechanistic and structural studies on Rhodococcus ATCC 39484 nitrilase.

Stevenson DE, Feng R, Dumas F, Groleau D, Mihoc A, Storer AC.

National Research Council of Canada, Biotechnology Research Institute, Montreal,
Quebec.

Rhodococcus ATCC 39484 produced a nitrilase when induced with isovaleronitrile. The enzyme was obtainable pure in milligram amounts, had a subunit Mr of 40 kDa, and demonstrated a substrate-induced activation related to aggregation of subunits to form a 560-kDa complex. The enzyme had a broad substrate specificity, had a pH optimum of 7.5, was stable up to 40 degrees C, and had one disulfide bridge and two free cysteine residues, one of which appeared to be catalytically essential. The N-terminal sequence was determined and found to have 78.3% homology, in a 23-residue overlap, with Klebsiella ozaenae nitrilase. The enzyme was inhibited competitively by benzylamine and benzaldehyde and irreversibly by benzyl bromide. However, benzyl bromide was shown to be nonspecific, causing multiple alkylation. Acid quenching of enzyme-substrate mixtures allowed for the detection of covalent enzyme-substrate complexes using mass spectrometry. The

covalent intermediate is suggested to be either a thioimidate or an acylenzyme and a reaction mechanism consistent with this observation and also the inhibitor results is proposed. The rate of breakdown of the covalent intermediates was found to be rate limiting even for substrates with undetectable rates of hydrolysis or those with very slow rates of intermediate formation. For phenylacetonitrile, a poor substrate, in addition to acid, approximately 2% of the product was the corresponding amide. This result suggests that a tetrahedral intermediate is formed which, for selected substrates, can break down anomalously to produce amide in place of the normal acid product. Under the conditions used in this study all other substrates tested were converted to acid.

PMID: 1388821 [PubMed - indexed for MEDLINE]

5: Eur J Biochem. 1990 Dec 27;194(3):765-72.

A novel nitrilase, arylacetonitrilase, of Alcaligenes faecalis JM3. Purification
and characterization.

Nagasawa T, Mauger J, Yamada H.

Department of Agricultural Chemistry, Kyoto University, Japan.

A new type of nitrilase, arylacetonitrilase, has been purified from isovaleronitrile-induced cells of Alcaligenes faecalis JM3 in four steps. The purity of the enzyme was confirmed by SDS/polyacrylamide gel electrophoresis, ampholyte electrofocusing and double immunodiffusion in agarose. The enzyme has a molecular mass of about 275 kDa and consists of six subunits of identical molecular mass. The purified enzyme exhibits a pH optimum of 7.5 and a temperature optimum of 45 degrees C. The enzyme is specific for arylacetonitriles such as 2-thiophenacetonitrile, p-tolyacetonitrile, p-chlorobenzylcyanide, p-fluorobenzylcyanide and 3-pyridylacetonitrile. The enzyme stoichiometrically catalyzes the hydrolysis of arylacetonitrile to arylacetic acid and ammonia, no formation of amide occurring. However, the enzyme does not attack nitrile groups attached to aromatic and heteroaromatic rings, which are hydrolyzed preferably by the nitrilases known previously. The enzyme requires thiol compounds such as dithiothreitol and 2-mercaptoethanol to exhibit its maximum activity.

PMID: 2269298 [PubMed - indexed for MEDLINE]

6: J Bacteriol. 1990 Sep;172(9):4807-15.

Purification and characterization of a novel nitrilase of Rhodococcus rhodochrous K22 that acts on aliphatic nitriles.

Kobayashi M, Yanaka N, Nagasawa T, Yamada H.

Department of Agricultural Chemistry, Faculty of Agriculture, Kyoto University,
Japan.

A novel nitrilase that preferentially catalyzes the hydrolysis of aliphatic nitriles to the corresponding carboxylic acids and ammonia

was found in the cells of a facultative crotononitrile-utilizing actinomycete isolated from soil. The strain was taxonomically studied and identified as Rhodococcus rhodochrous. The nitrilase was purified, with 9.08% overall recovery, through five steps from a cell extract of the stain. After the last step, the purified enzyme appeared to be homogeneous, as judged by polyacrylamide gel electrophoresis, analytical centrifugation, and double immunodiffusion in agarose. The relative molecular weight values for the native enzyme, estimated from the ultracentrifugal equilibrium and by high-performance liquid chromatography, were approximately 604,000 +/- 30,000 and 650,000, respectively, and the enzyme consisted of 15 to 16 subunits identical in molecular weight (41,000). The enzyme acted on aliphatic olefinic nitriles such as crotononitrile and acrylonitrile as the most suitable substrates. The apparent Km values for crotononitrile and acrylonitrile were 18.9 and 1.14 mM, respectively. The nitrilase also catalyzed the direct hydrolysis of saturated aliphatic nitriles, such as valeronitrile, 4-chlorobutyronitrile, and glutaronitrile, to the corresponding acids without the formation of amide intermediates. Hence, the R. rhodochrous K22 nitrilase is a new type distinct from all other nitrilases that act on aromatic and related nitriles.

PMID: 2394676 [PubMed - indexed for MEDLINE]

7: Eur J Biochem. 1989 Jun 15;182(2):349-56.

Nitrilase of Rhodococcus rhodochrous J1. Purification and characterization.

Kobayashi M, Nagasawa T, Yamada H.

Department of Agricultural Chemistry, Faculty of Agriculture, Kyoto University,
Japan.

Nitrilase was purified from an extract of isovaleronitrile-induced cells of Rhodococcus rhodochrous J1 in seven steps. In the last step, the enzyme was crystallized by adding ammonium sulfate. The crystallized enzyme appeared to be homogeneous by polyacrylamide electrophoresis, ampholyte electrofocusing and double immunodiffusion in agarose. The enzyme has a molecular mass of about 78 kDa and consists of two subunits identical in molecular mass. The purified enzyme exhibits a pH optimum of 7.6 and a temperature optimum of 45 degrees C. The enzyme catalyzed stoichiometrically the hydrolysis of benzonitrile to benzoic acid and ammonia, and no formation of amide was detected. The enzyme required thiol compounds such as dithiothreitol, L-cysteine or reduced glutathione to exhibit maximum activity. The enzyme was specific for nitrile groups attached to an aromatic or heteroaromatic ring, e.g. benzonitrile, 3-chlorobenzonitrile, 4-tolunitrile, 2-furonitrile and 2-thiophenecarbonitrile. The comparison of the properties of the enzyme with other nitrilases and nitrile hydratases has been also discussed.

PMID: 2737207 [PubMed - indexed for MEDLINE]

8: Ciba Found Symp. 1988;140:16-31.

Microbial hydrolysis of organic nitriles and amides.

Ingvorsen K, Yde B, Godtfredsen SE, Tsuchiya RT.

Novo Industri A/S, Biochemical Synthesis Group, Bagsvaerd, Denmark.

Nitrile-hydrating enzymes produced by bacteria and fungi catalyse the conversion of a large number of chemically diverse nitriles, including many economically important compounds used industrially for chemical synthesis of amides and acids. This paper presents data on two new, highly different nitrile-hydrolysing enzymes which were isolated in connection with our studies on enzymic nitrile transformations. Particular attention was paid to the enzymes' substrate specificities and sensitivity to substrate/product inhibition. One of our microbial isolates was a Rhodococcus sp. (strain CH5). This strain produces a constitutive hydratase that has a broad substrate spectrum, including aliphatic and aromatic nitriles, mononitriles and dinitriles, hydroxynitriles and amino-nitriles. It also produces a constitutive amidase of equally low substrate specificity. The hydratase/amidase system catalysed the hydrolysis of D,L-aminonitriles into racemic mixtures of amino acids. Strain CH5 is able to produce high concentrations of malonic acid monoamide from malononitrile and malonamide. The other isolate, Alcaligenes sp. (strain I4), can convert high concentrations of cyanoacetate into malonic acid, presumably by means of an aliphatic nitrilase that is specific for cyanoacetate. Enzyme kinetic experiments have shown that this enzyme is very resistant to both substrate and product inhibition.

Publication Types:
    Review
    Review, Tutorial

PMID: 3073055 [PubMed - indexed for MEDLINE]

9: Int J Biochem. 1985;17(6):677-83.

Characterization of a nitrilase from Nocardia sp. (Rhodochrous group) N.C.I.B.
11215, using p-hydroxybenzonitrile as sole carbon source.

Harper DB.

The purification and properties of an enzyme from Nocardia sp. which catalyses the conversion of p-hydroxybenzonitrile to p-hydroxybenzoic acid and ammonia without intermediate formation of the amide is described. The enzyme displayed a broad pH optimum between 7.0 and 9.5 and exhibited Michaelis-Menten kinetics with Km of 1.27 mM for p-hydroxybenzonitrile. The 12-unit multimeric enzyme possessed a mol. wt of 560,000 and was sensitive to thiol-specific reagents. Although aliphatic nitriles were not substrates for the enzyme a broad range of substituted aromatic nitriles were attacked with a general preference being shown for those with meta substitution.

PMID: 4029486 [PubMed - indexed for MEDLINE]

10: J Biol Chem. 1964 Dec;239:4257-62.

RICININE NITRILASE. I. REACTION PRODUCT AND SUBSTRATE SPECIFICITY.

ROBINSON WG, HOOK RH.

PMID: 14247679 [PubMed - OLDMEDLINE for Pre1966]

11: Arch Biochem Biophys. 1964 Jul;107:62-8.

NITRILASE. II. SUBSTRATE SPECIFICITY AND POSSIBLE MODE OF ACTION.

MAHADEVAN S, THIMANN KV.

PMID: 14211567 [PubMed - OLDMEDLINE for Pre1966]

Abstract
The action of the nitrilase from barley leaves on 26 nitriles has been studied. p-Hydroxy and p-amino benzonitriles and 3-cyanopyridine were shown chromatographically to yield the corresponding carboxylic acids, and conversion of α-naphthaleneacetonitrile to α-naphthaleneacetic acid was shown by bioassay. The enzyme is thus not highly specific. The moderate biological activity of 2,4-dichlorophenoxyacetonitrile in pea stems, which do not contain nitrilase, is shown, both from biochemical considerations and from comparative bioassay, to be probably due to relatively slow nonenzymatic hydrolysis.

Hydrolysis rates for a series of substituted benzonitriles lead to the conclusion that electron-withdrawing ring substituents favor hydrolysis, electron-donating substituents retard it. The enzymatic hydrolysis more nearly resembles chemical hydrolysis with alkali rather than that with acid. Enzymatic hydrolysis of indole, pyridine and imidazole nitriles, as well as of 5 aliphatic nitriles, agrees in general with the above interpretation, and some of the exceptions are accounted for by steric hindrance.

The reaction mechanism is considered to involve nucleophilic attack on the fractionally positive C atom of the nitrile, which remains enzyme-bound throughout. A scheme commencing with attack by an SH group of the enzyme is suggested.

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REFERENCE   1  (residues 1 to 339)
  AUTHORS   Bartel,B. and Fink,G.R.
  TITLE     Differential regulation of an auxin-producing nitrilase
gene family
            in Arabidopsis thaliana
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (14), 6649-6653 (1994)
   PUBMED   8022831
REFERENCE   2  (residues 1 to 339)
  AUTHORS   Bartel,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-1994) Bonnie Bartel, Whitehead Institute
for
            Biomedical research, Nine Cambridge Center, Cambridge, MA
02142,
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FEB-1999
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            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1  (residues 1 to 349)
  AUTHORS   Tsunoda,H. and Yamaguchi,K.
  TITLE     The cDNA sequence of an auxin-producing nitrilase homolog
in
            Tobacco
  JOURNAL   Plant Physiol. 109, 339 (1995)
REFERENCE   2  (residues 1 to 349)
  AUTHORS   Tsunoda,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-1995) Hiroyuki Tsunoda, Kanazawa
University,
            Institute for Gene Research; Takaramachi 13-1, Kanazawa,
Ishikawa
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FEB-1999
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REFERENCE 1 (residues 1 to 366)
AUTHORS Kobayashi,M., Komeda,H., Yanaka,N., Nagasawa,T. and
Yamada,H.
TITLE Nitrilase from Rhodococcus rhodochrous J1. Sequencing and
overexpression of the gene and identification of an
essential
cysteine residue
JOURNAL J. Biol. Chem. 267 (29), 20746-20751 (1992)
PUBMED 1400390
REFERENCE 2 (residues 1 to 366)
AUTHORS Kobayashi,M.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1992) Michihiko Kobayashi, Kyoto
University,
Department of Agricultural Chemistry, Faculty of
Agriculture;
Oiwake-tyo, Kitashirakawa, Sakyo-ku, Kyoto, Kyoto 606,
Japan
(Tel:075-753-6114, Fax:075-753-6128)
COMMENT Submitted (10-Jun-1992) to DDBJ by:
Michihiko Kobayashi
Department of Agricultural Chemistry
Kyoto University
Kitashirakawa-oiwakecho
Sakyo-ku, Kyoto 606-01
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JUL-1994
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  TITLE     Differential regulation of an auxin-producing nitrilase
gene family
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  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 348)
  AUTHORS   Tsunoda,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-1996) Hiroyuki Tsunoda, Institute for
Gene
            Research, Kanazawa University; Takaramachi 1-13, Kanazawa,
Ishikawa
            920, Japan (E-mail:mukai@kenroku.ipc.kanazawa-u.ac.jp,
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Tel:0762-62-8151(ex.5886), Fax:0762-62-2230)
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VERSION AAB05220.1 GI:1469912
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ORGANISM Arabidopsis thaliana
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 4 (residues 1 to 339)
AUTHORS Zhou,L., Bartel,B. and Thornburg,R.W.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1995) Robert W. Thornburg, Biochemistry and
Biophysics, Iowa State University, 2212 Molecular Biology Building,
Ames, IA 50011, USA

```
COMMENT     On Aug 1, 1996 this sequence version replaced gi:1245120.
FEATURES             Location/Qualifiers
     source          1..339
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
                     /chromosome="III"
                     /map="between GL1 and m249"
                     /ecotype="Col-0 (Columbia)"
     Protein         1..339
                     /product="nitrilase 2"
                     /EC_number="3.5.5.1"
                     /function="catalyzes the conversion of IAN into
IAA"
     CDS             1..339
                     /gene="NIT2"

                     /coded_by="join(U38845.1:1795..1904,U38845.1:1976..2154,
                     U38845.1:2702..2995,U38845.1:3088..3369,
                     U38845.1:3462..3616)"
                     /note="nitrile aminohydrolase"
ORIGIN
        1 mstsentpfn gvasstivra tivqastvyn dtpatlgkan kfiveaatkg
selvvfpeaf
       61 iggyprgfrf glgvgvhnee grdefrkyha saikvpgpev eklaelagkn
nvylvmgaie
      121 kdgytlycta lffspqgqfl gkhrklmpts lerciwgqgd gstipvydtp
igklgaaicw
      181 enrmplyrta lyakgielyc aptadgskew qssmlhiaie ggcfvlsacq
fclrkdfpdh
      241 pdylftdwyd dkepdsivsq ggsviisplg qvlagpnfes eglitadldl
gdvaraklyf
      301 dsvghysrpd vlhltvnehp kkpvtfiskv ekaeddsnk
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LOCUS       AAC40184                323 aa            linear   ROD 22-
JUL-1998
DEFINITION  nitrilase homolog 1 [Mus musculus].
ACCESSION   AAC40184
VERSION     AAC40184.1  GI:3242980
DBSOURCE    locus AF069985 accession AF069985.1
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (residues 1 to 323)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.H.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Nitrilase and Fhit homologs are encoded as fusion proteins
in
            Drosophila melanogaster and Caenorhabditis elegans
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8744-8749 (1998)
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   PUBMED   9671749
REFERENCE   2  (residues 1 to 323)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1998) Kimmel Cancer Inst., Thomas
Jefferson
            Univ., 233 S. Tenth St., Philadelphia, PA 19107, USA
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..323
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="1"
                     /map="1q21-q23"
     Protein         1..323
                     /product="nitrilase homolog 1"
                     /name="Nit1"
     CDS             1..323
                     /gene="Nit1"

/coded_by="join(AF069985.1:605..606,AF069985.1:1177..1263,
                     AF069985.1:1638..1889,AF069985.1:2015..2118,
                     AF069985.1:2362..2495,AF069985.1:2626..2751,
                     AF069985.1:3392..3658)"
                     /note="alternatively spliced"
ORIGIN
        1 mlgfitrpph qllctgyrll ripvlctqpr prtmssstsw elplvavcqv
tstpnkqenf
       61 ktcaelvqea arlgaclafl peafdfiarn paetlllsep lngdllgqys
qlarecgiwl
      121 slggfhergq dweqnqkiyn chvllnskgs vvasyrkthl cdveipgqgp
mresnytkpg
      181 gtleppvktp agkvglaicy dmrfpelslk laqagaeilt ypsafgsvtg
pahwevllra
      241 raiesqcyvi aaaqcgrhhe trasyghsmv vdpwgtvvar csegpglcla
ridlhflqqm
      301 rqhlpvfqhr rpdlygslgh pls
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LOCUS       AAC39137                 460 aa            linear   INV 22-
JUL-1998
DEFINITION  nitrilase and fragile histidine triad fusion protein
NitFhit
            [Drosophila melanogaster].
ACCESSION   AAC39137
VERSION     AAC39137.1  GI:3228670
DBSOURCE    locus AF069989 accession AF069989.1
KEYWORDS    .
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (residues 1 to 460)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.H.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Nitrilase and Fhit homologs are encoded as fusion proteins
in
            Drosophila melanogaster and Caenorhabditis elegans
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8744-8749 (1998)
   PUBMED   9671749
REFERENCE   2  (residues 1 to 460)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1998) Kimmel Cancer Inst., Thomas
Jefferson
            Univ., 233 S. Tenth St., Philadelphia, PA 19107, USA
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..460
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /chromosome="3"
                     /map="61A"
     Protein         1..460
                     /product="nitrilase and fragile histidine triad
fusion
                     protein NitFhit"
     CDS             1..460
                     /gene="NitFhit"
                     /coded_by="AF069989.1:44..1426"
ORIGIN
        1 mstlvnttrr siviaihqql rrmsvqkrkd qsatiavgqm rstsdkaanl
sqvielvdra
       61 ksqnacmlfl peccdfvges rtqtielseg ldgelmaqyr elakcnkiwi
slggvhernd
      121 qkifnahvll nekgelaavy rklhmfdvtt kevrlresdt vtpgyclerp
vstpvgqigl
      181 qicydlrfae pavllrklga nlltypsaft yatgkahwei llraraietq
cfvvaaaqig
      241 whnqkrqswg hsmivspwgn vladcseqel digtaevdls vlqslyqtmp
cfehrrndiy
      301 altaynlrsk eptqdrpfat nivdkrtify esehcfaftn lrcvvkghvl
vstkrvtprl
      361 cgldcaemad mfttvclvqr llekiyqtts atvtvqdgaq agqtvphvhf
himprrlgdf
      421 ghndqiyvkl deraeekppr tieerieeaq iyrkfltdis
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LOCUS       AAC40185                323 aa            linear   ROD 22-
JUL-1998
DEFINITION  nitrilase 1 [Mus musculus].
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ACCESSION   AAC40185
VERSION     AAC40185.1  GI:3228668
DBSOURCE    locus AF069988 accession AF069988.1
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (residues 1 to 323)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.H.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Nitrilase and Fhit homologs are encoded as fusion proteins
in
            Drosophila melanogaster and Caenorhabditis elegans
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8744-8749 (1998)
   PUBMED   9671749
REFERENCE   2  (residues 1 to 323)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1998) Kimmel Cancer Inst., Thomas
Jefferson
            Univ., 233 S. Tenth St., Philadelphia, PA 19107, USA
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..323
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="1"
                     /map="1q21-q23"
     Protein         1..323
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     CDS             1..323
                     /gene="Nit1"
                     /coded_by="AF069988.1:58..1029"
ORIGIN
        1 mlgfitrpph qllctgyrll rtpvlctqpr prtmssstsw elplvavcqv
tstpnkqenf
       61 ktcaelvqea arlgaclafl peafdfiarn paetlllsep lngdllgqys
qlarecgiwl
      121 slggfhergq dweqnqkiyn chvllnskgs vvasyrkthl cdveipgqgp
mresnytkpg
      181 gtleppvktp agkvglaicy dmrfpelslk laqagaeilt ypsafgsvtg
pahwevllra
      241 raiesqcyvi aaaqcgrhhe trasyghsmv vdpwgtvvar csegpglcla
ridlhflqqm
      301 rqhlpvfqhr rpdlygslgh pls
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LOCUS       AAC39907                 327 aa            linear   PRI 22-
JUL-1998
DEFINITION  nitrilase 1 [Homo sapiens].
ACCESSION   AAC39907
VERSION     AAC39907.1  GI:3228666
DBSOURCE    locus AF069987 accession AF069987.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (residues 1 to 327)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.H.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Nitrilase and Fhit homologs are encoded as fusion proteins
in
            Drosophila melanogaster and Caenorhabditis elegans
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8744-8749 (1998)
   PUBMED   9671749
REFERENCE   2  (residues 1 to 327)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1998) Kimmel Cancer Inst., Thomas
Jefferson
            Univ., 233 S. Tenth St., Philadelphia, PA 19107, USA
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..327
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     Protein         1..327
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                     /name="Nit1"
     CDS             1..327
                     /gene="NIT1"
                     /coded_by="AF069987.1:77..1060"
ORIGIN
        1 mlgfitrpph rflsllcpgl ripqlsvlca qprpramais sssceIplva
vcqvtstpdk
       61 qqnfktcael vreaarlgac laflpeafdf iardpaetlh lseplggkll
eeytqlarec
      121 glwlslggfh ergqdweqtq kiynchvlln skgavvatyr kthlcdveip
gqgpmcesns
      181 tmpgpslesp vstpagkigl avcydmrfpe lslalaqaga eiltypsafg
sitgpahwev
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      241 llraraietq cyvvaaaqcg rhhekrasyg hsmvvdpwgt vvarcsegpg
lclaridlny
      301 lrqlrrhlpv fqhrrpdlyg nlghpls
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LOCUS       AAC39136                 440 aa            linear   INV 22-
JUL-1998
DEFINITION  nitrilase and fragile histidine triad fusion protein
NitFhit
            [Caenorhabditis elegans].
ACCESSION   AAC39136
VERSION     AAC39136.1  GI:3228664
DBSOURCE    locus AF069986 accession AF069986.1
KEYWORDS    .
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (residues 1 to 440)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.H.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Nitrilase and Fhit homologs are encoded as fusion proteins
in
            Drosophila melanogaster and Caenorhabditis elegans
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8744-8749 (1998)
   PUBMED   9671749
REFERENCE   2  (residues 1 to 440)
  AUTHORS   Pekarsky,Y., Campiglio,M., Siprashvili,Z., Druck,T.,
Sedkov,Y.,
            Tillib,S., Draganescu,A., Wermuth,P., Rothman,J.,
Huebner,K.,
            Buchberg,A.M., Mazo,A., Brenner,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1998) Kimmel Cancer Inst., Thomas
Jefferson
            Univ., 233 S. Tenth St., Philadelphia, PA 19107, USA
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..440
                     /organism="Caenorhabditis elegans"
                     /db_xref="taxon:6239"
     Protein         1..440
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fusion
                     protein NitFhit"
     CDS             1..440
                     /gene="NitFhit"
                     /coded_by="AF069986.1:3..1325"
ORIGIN
        1 mlstvfrrtm atgrhfiavc qmtsdndlek nfqaaknmie ragekkcemv
flpecfdfig
       61 lnkneqidla matdceymek yrelarkhni wlslgglhhk dpsdaahpwn
thliidsdgv
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      121 traeynklhl fdleipgkvr lmesefskag temippvdtp igrlglsicy
dvrfpelslw
      181 nrkrgaqlls fpsaftlntg lahwetllra raienqcyvv aaaqtgahnp
krqsyghsmv
      241 vdpwgavvaq cservdmcfa eidlsyvdtl remqpvfshr rsdlytlhin
ekssetgglk
      301 farfnipadh ifystphsfv fvnlkpvtdg hvlvspkrvv prltdltdae
tadlfivakk
      361 vqamlekhhn vtstticvqd gkdagqtvph vhihilprra gdfgdneiyq
klashdkepe
      421 rkprsneqma eeavvyrnlm
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LOCUS       AAB05221                 346 aa            linear   PLN 31-
JUL-1996
DEFINITION  nitrilase 1.
ACCESSION   AAB05221
VERSION     AAB05221.1  GI:1389699
DBSOURCE    locus ATU38845 accession U38845.1
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   4  (residues 1 to 346)
  AUTHORS   Zhou,L., Bartel,B. and Thornburg,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1995) Robert W. Thornburg, Biochemistry
and
            Biophysics, Iowa State University, 2212 Molecular Biology
Building,
            Ames, IA 50011, USA
FEATURES             Location/Qualifiers
     source          1..346
                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
                     /chromosome="III"
                     /map="between GL1 and m249"
                     /ecotype="Col-0 (Columbia)"
     Protein         1..346
                     /product="nitrilase 1"
                     /EC_number="3.5.5.1"
                     /function="catalyzes the conversion of IAN into
IAA"
     CDS             1..346
                     /gene="NIT1"

/coded_by="join(U38845.1:5343..5472,U38845.1:5565..5744,
                     U38845.1:6374..6667,U38845.1:6761..7042,
                     U38845.1:7127..7281)"
                     /note="nitrile aminohydrolase"
ORIGIN
        1 msstkdmstv qnatpfngva psttvrvtiv qsstvyndtp atidkaekyi
veaaskgael
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       61 vlfpegfigg yprgfrfgla vgvhneegrd efrkyhasai hvpgpevarl
advarknhvy
      121 lvmgaiekeg ytlyctvlff spqgqflgkh rklmptsler ciwgqgdgst
ipvydtpigk
      181 lgaaicwenr mplyrtalya kgielycapt adgskewqss mlhiaieggc
fvlsacqfcq
      241 rkhfpdhpdy lftdwyddke hdsivsqggs viisplgqvl agpnfesegl
vtadidlgdi
      301 araklyfdsv ghysrpdvlh ltvnehprks vtfvtkveka eddsnk

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LOCUS       AAE06465                 344 aa            linear   PAT 29-
SEP-1999
DEFINITION  Sequence 1 from patent US 5872000.
ACCESSION   AAE06465
VERSION     AAE06465.1  GI:5953961
DBSOURCE    accession AAE06465.1
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (residues 1 to 344)
  AUTHORS   Yu,F.
  TITLE     Nitrilase gene
  JOURNAL   Patent: US 5872000-A 1 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..344
                     /organism="unknown"
ORIGIN
        1 xttdysgtfk aavtqaepvw fdlsatvdkt ialveeasra gadliafpet
wipgypwflw
       61 ldsvawqsqy firypqnsld ldgsefaair eaarkndiai tmgfserghg
slymgqavie
      121 rdgvvvrtrr klkpthvert lfgegdgsdl vvdqtslgrv gslccwehlq
pltkyamysq
      181 heqihiaawp sfsifpgavy algpevntaa sqqyavegqt yvlapcavig
dagweafadt
      241 eekrqlihkg ggyariygpd grslaeplap ndegilyadi dlsailaakn
padpvghysr
      301 pdvlrlgfnk apqpkvnilg tepsrttstq crpttirrsw rfpe
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LOCUS       CAA02248                 354 aa            linear   UNA 05-
MAR-1997
DEFINITION  unnamed protein product [unidentified].
ACCESSION   CAA02248
VERSION     CAA02248.1  GI:2294001
DBSOURCE    embl accession A36733.1
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (residues 1 to 354)
  AUTHORS   Petre,D., Cerbelaud,E., Levy-Schil,S. and Crouzet,J.
  TITLE     Recombinant nitrilase and use thereof
  JOURNAL   Patent: EP 0596812-A 11-MAY-1994;
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            RHONE POULENC CHIMIE (FR)
COMMENT     Other publication JP 7051070 950228
            Other publication CA 2103616 940211
            Other publication FR 2694571 940211
            Other publication BR 9305280 940628.
FEATURES                Location/Qualifiers
     source             1..354
                        /organism="unidentified"
                        /db_xref="taxon:32644"
     Protein            1..354
                        /name="unnamed protein product"
     CDS                1..354
                        /coded_by="A36733.1:87..1151"
ORIGIN
        1 mknyptvkva avqaapvfmn leatvdktck liaeaasmga kvigfpeafi
pgypywiwts
       61 nmdftgmmwa vlfknaieip skevqqisda akkngvyvcv svsekdnasl
yltqlwfdpn
      121 gnligkhrkf kptsseravw gdgdgsmapv fkteygnlgg lqcwehalpl
niaamgslne
      181 qvhvaswpaf vpkgavssrv sssvcastna mhqiisqfya isnqvyvims
tnlvgqdmid
      241 migkdefskn flplgsgnta iisntgeila sipqdaegia vaeidlnqii
ygkwlldpag
      301 hystpgflsl tfdqsehvpv kkigeqtnhf isyedlhedk mdmltipprr vata
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